

HCOO<sup>-1</sup>." with --SO<sub>4</sub><sup>2-</sup>, PO<sub>4</sub><sup>3-</sup>, Cl<sup>-</sup> and HCOO<sup>-</sup>---.

On page 119, on lines 13-17, after please replace "U.S. Patent App. Ser. No. 627,795 filed July 5, 1984, continuation filed June 4, 1987 (serial no. not yet assigned) and Ser. No. 816,711 filed January 7, 1986, which are both entitled ACCELERATED NUCLEIC ACID REASSOCIATION METHOD." with --U.S. Patent 5,132,207.---

In the Claims:

Please cancel claims 1-30 without prejudice to future prosecution.

Please add claims as follows:

330. (New) A method of selecting an oligonucleotide probe sequence able to distinguish one or more target species of a genus from at least one nontarget species belonging to said genus comprising the steps of:

a) aligning a variable region present in nucleic acid of said one or more target species and nucleic acid of said at least one nontarget species to identify a variable sequence, wherein said variable region is present in a target region corresponding to either  
bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;  
bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;  
bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;  
bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;  
bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;  
bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;  
bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;  
bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;  
bases 980-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;  
bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;  
bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;  
bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1440-1620 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and  
bases 2190-2335 of *E. coli* 23S rRNA or the encoding DNA; and

b) designing said oligonucleotide probe sequence so that a duplex formed between an oligonucleotide comprising said oligonucleotide probe sequence forms a probe:target duplex with nucleic acid from said one or more target species having a higher  $T_m$  than a probe:non-target duplex formed between said oligonucleotide and nucleic acid from said at least one non-target species.

331. (New) The method of claim 330, wherein said target region corresponds to either bases 65-108 of *E. coli* 5S rRNA or the encoding DNA.

332. (New) The method of claim 331, wherein said target region corresponds to bases 65-108 of *E. coli* 5S rRNA.

333. (New) The method of claim 331 wherein said genus is *Mycoplasma*.

334. (New) The method of claim 332 wherein said genus is *Mycoplasma*.

335. (New) The method of claim 330, wherein said target region corresponds to either bases 60-105 of *E. coli* 16S rRNA or the encoding DNA.

336. (New) The method of claim 335, wherein said target region corresponds to bases 60-105 of *E. coli* 16S rRNA.

337. (New) The method of claim 335, wherein said genus is *Chlamydia*.

338. (New) The method of claim 336, wherein said genus is *Chlamydia*.

339. (New) The method of claim 330, wherein said target region corresponds to either bases 120-150 of *E. coli* 16S rRNA or the encoding DNA.

340. (New) The method of claim 339, wherein said target region corresponds to bases 120-150 of *E. coli* 16S rRNA.

341. (New) The method of claim 339, wherein said genus is *Neisseria*.

342. (New) The method of claim 341, wherein said target region corresponds to bases 125-150 of *E. coli* 16S rRNA.

343. (New) The method of claim 330, wherein said target region corresponds to either bases 170-230 of *E. coli* 16S rRNA or the encoding DNA.

344. (New) The method of claim 343, wherein said target region corresponds to bases 170-230 of *E. coli* 16S rRNA.

345. (New) The method of claim 343, wherein said genus is *Mycobacterium* and said target region corresponds to either bases 185-225 of *E. coli* 16S rRNA or the encoding DNA.

346. (New) The method of claim 345, wherein said target region corresponds to bases 185-225 of *E. coli* 16S rRNA.

347. (New) The method of claim 343, wherein said genus is *Chlamydia* and said target region corresponds to either bases 175-210 of *E. coli* 16S rRNA or the encoding DNA.

348. (New) The method of claim 347, wherein said target region corresponds to bases 175-210 of *E. coli* 16S rRNA.

349. (New) The method of claim 343, wherein said genus is *Mycoplasma* and said target region corresponds to either bases 190-230 of *E. coli* 16S rRNA or the encoding DNA.

350. (New) The method of claim 349, wherein said target region corresponds to bases 190-230 of *E. coli* 16S rRNA.

351. (New) The method of claim 330, wherein said target region corresponds to either bases 405-490 of *E. coli* 16S rRNA or the encoding DNA.

352. (New) The method of claim 351, wherein said target region corresponds to bases 405-490 of *E. coli* 16S rRNA.

353. (New) The method of claim 351, wherein said genus is Mycoplasma and said target region corresponds to either bases 450-490 of *E. coli* 16S rRNA or the encoding DNA.

354. (New) The method of claim 353, wherein said target region corresponds to bases 450-490 of *E. coli* 16S rRNA.

355. (New) The method of claim 351, wherein said genus is Neisseria and said target region corresponds to either bases 455-485 of *E. coli* 16S rRNA or the encoding DNA.

356. (New) The method of claim 355, wherein said target region corresponds to bases 455-485 of *E. coli* 16S rRNA.

357. (New) The method of claim 330, wherein said target region corresponds to either bases 600-675 of *E. coli* 16S rRNA or the encoding DNA.

358. (New) The method of claim 357, wherein said target region corresponds to bases 600-675 of *E. coli* 16S rRNA.

359. (New) The method of claim 357, wherein said genus is Chlamydia and said target region corresponds to either bases 600-635 of *E. coli* 16S rRNA or the encoding DNA.

360. (New) The method of claim 359, wherein said target region corresponds to bases 600-635 of *E. coli* 16S rRNA.

361. (New) The method of claim 330, wherein said target region corresponds to either bases 705-735 of *E. coli* 16S rRNA or the encoding DNA.

362. (New) The method of claim 361, wherein said target region corresponds to bases 705-735 of *E. coli* 16S rRNA.

363. (New) The method of claim 330, wherein said target region corresponds to either bases 820-870 of *E. coli* 16S rRNA or the encoding DNA.

364. (New) The method of claim 363, wherein said target region corresponds to bases 820-870 of *E. coli* 16S rRNA.

365. (New) The method of claim 363, wherein said genus is *Chlamydia* and said target region corresponds to either bases 830-870 of *E. coli* 16S rRNA or the encoding DNA.

366. (New) The method of claim 365, wherein said target region corresponds to bases 830-870 of *E. coli* 16S rRNA.

367. (New) The method of claim 363, wherein said genus is *Mycoplasma* and said target region corresponds to either bases 820-860 of *E. coli* 16S rRNA or the encoding DNA.

368. (New) The method of claim 367, wherein said target region corresponds to bases 820-860 of *E. coli* 16S rRNA.

369. (New) The method of claim 363, wherein said genus is Streptococcus and said target region corresponds to either bases 825-860 of *E. coli* 16S rRNA or the encoding DNA.

370. (New) The method of claim 369, wherein said target region corresponds to bases 825-860 of *E. coli* 16S rRNA.

371. (New) The method of claim 330, wherein said target region corresponds to either bases 980-1060 of *E. coli* 16S rRNA or the encoding DNA.

372. (New) The method of claim 371, wherein said target region corresponds to bases 980-1060 of *E. coli* 16S rRNA.

373. (New) The method of claim 371, wherein said genus is Escherichia and said target region corresponds to either bases 995-1030 of *E. coli* 16S rRNA or the encoding DNA.

374. (New) The method of claim 373, wherein said target region corresponds to bases 995-1030 of *E. coli* 16S rRNA.

375. (New) The method of claim 371, wherein said genus is Neisseria and said target region corresponds to either bases 980-1015 of *E. coli* 16S rRNA or the encoding DNA.

376. (New) The method of claim 375, wherein said target region corresponds to bases 980-1015 of *E. coli* 16S rRNA.

377. (New) The method of claim 330, wherein said target region corresponds to either bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA.

378. (New) The method of claim 377, wherein said target region corresponds to bases 1125-1155 of *E. coli* 16S rRNA.

379. (New) The method of claim 330, wherein said target region corresponds to either bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA.

380. (New) The method of claim 379, wherein said target region corresponds to bases 1250-1290 of *E. coli* 16S rRNA.

381. (New) The method of claim 379, wherein said genus is *Mycoplasma* and said target region corresponds to either bases 1255-1290 of *E. coli* 16S rRNA or the encoding DNA.

382. (New) The method of claim 381, wherein said target region corresponds to bases 1255-1290 of *E. coli* 16S rRNA.

383. (New) The method of claim 330, wherein said target region corresponds to either bases 270-405 of *E. coli* 23S rRNA or the encoding DNA.

384. (New) The method of claim 383, wherein said target region corresponds to bases 270-405 of *E. coli* 23S rRNA.



385. (New) The method of claim 383, wherein said genus is Chlamydia and said target region corresponds to either bases 275-320 of *E. coli* 23S rRNA or the encoding DNA.

386. (New) The method of claim 385, wherein said target region corresponds to bases 275-320 of *E. coli* 23S rRNA.

387. (New) The method of claim 383, wherein said genus is Chlamydia and said target region corresponds to either bases 330-365 of *E. coli* 23S rRNA or the encoding DNA.

388. (New) The method of claim 387, wherein said target region corresponds to bases 330-365 of *E. coli* 23S rRNA.

389. (New) The method of claim 383, wherein said genus is *Proteus* and said target region corresponds to either bases 270-305 of *E. coli* 23S rRNA or the encoding DNA.

390. (New) The method of claim 389, wherein said target region corresponds to bases 270-305 of *E. coli* 23S rRNA.

391. (New) The method of claim 383, wherein said genus is *Pseudomonas* and said target region corresponds to either bases 365-405 of *E. coli* 23S rRNA or the encoding DNA.

392. (New) The method of claim 391, wherein said target region corresponds to bases 365-405 of *E. coli* 23S rRNA.

393. (New) The method of claim 383, wherein said genus is Enterobacter and said target region corresponds to either bases 305-340 of *E. coli* 23S rRNA or the encoding DNA.

394. (New) The method of claim 393, wherein said target region corresponds to bases 305-340 of *E. coli* 23S rRNA.

395. (New) The method of claim 330, wherein said target region corresponds to either bases 535-575 of *E. coli* 23S rRNA or the encoding DNA.

396. (New) The method of claim 395, wherein said target region corresponds to bases 535-575 of *E. coli* 23S rRNA.

397. (New) The method of claim 395, wherein said genus is Mycobacterium and said target region corresponds to either bases 540-575 of *E. coli* 23S rRNA or the encoding DNA.

398. (New) The method of claim 397, wherein said target region corresponds to bases 540-575 of *E. coli* 23S rRNA.

399. (New) The method of claim 330, wherein said target region corresponds to either bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA.

400. (New) The method of claim 399, wherein said target region corresponds to bases 1150-1200 of *E. coli* 23S rRNA.

401. (New) The method of claim 399, wherein said genus is Mycobacterium and said target region corresponds to either bases 1155-1190 of *E. coli* 23S rRNA or the encoding DNA.

402. (New) The method of claim 401, wherein said target region corresponds to bases 1155-1190 of *E. coli* 23S rRNA.

403. (New) The method of claim 399, wherein said genus is Chlamydia and said target region corresponds to either bases 1160-1190 of *E. coli* 23S rRNA or the encoding DNA.

404. (New) The method of claim 403, wherein said target region corresponds to bases 1160-1190 of *E. coli* 23S rRNA.

405. (New) The method of claim 330, wherein said target region corresponds to either bases 1440-1620 of *E. coli* 23S rRNA or the encoding DNA.

406. (New) The method of claim 405, wherein said target region corresponds to bases 1440-1620 of *E. coli* 23S rRNA.

407. (New) The method of claim 405, wherein said genus is Chlamydia and said target region corresponds to either bases 1450-1490 of *E. coli* 23S rRNA or the encoding DNA.

408. (New) The method of claim 407, wherein said target region corresponds to bases 1450-1490 of *E. coli* 23S rRNA.

409. (New) The method of claim 405, wherein said genus is Chlamydia and said target region corresponds to either bases 1510-1545 of *E. coli* 23S rRNA or the encoding DNA.

410. (New) The method of claim 409, wherein said target region corresponds to bases 1510-1545 of *E. coli* 23S rRNA.

411. (New) The method of claim 330, wherein said target region corresponds to either bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA.

412. (New) The method of claim 411, wherein said target region corresponds to bases 1710-1750 of *E. coli* 23S rRNA.

413. (New) The method of claim 411, wherein said genus is Chlamydia.

414. (New) The method of claim 412, wherein said genus is Chlamydia.

415. (New) The method of claim 330, wherein said target region corresponds to either bases 2190-2335 of *E. coli* 23S rRNA or the encoding DNA.

416. (New) The method of claim 415, wherein said target region corresponds to bases 2190-2335 of *E. coli* 23S rRNA.

417. (New) The method of claim 415, wherein said genus is Mycobacterium and said target region corresponds to either bases 2195-2235 of *E. coli* 23S rRNA or the encoding DNA.

418. (New) The method of claim 417, wherein said target region corresponds to bases 2195-2235 of *E. coli* 23S rRNA.

419. (New) The method of any of claims 331-418, further comprising the steps of:

producing said oligonucleotide probe comprising said oligonucleotide probe sequence,

determining whether said oligonucleotide probe hybridizes to nucleic acid from said one or more target species under high stringency hybridization assay conditions to form a detectable probe:target duplex; and

determining whether said oligonucleotide probe hybridizes to nucleic acid from said at least one nontarget species under said conditions to form a detectable probe:nontarget duplex.

420. (New) A method of selecting an oligonucleotide probe sequence able to distinguish two or more target species belonging to a first genus from at least one nontarget species belonging to a second genus comprising the steps of:

a) aligning a variable region present in nucleic acid of said two or more target species and nucleic acid of said at least one nontarget species to identify a variable sequence, wherein said variable region is present in a target region corresponding to either  
bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;  
bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;  
bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;  
bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;  
bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;  
bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;  
bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;  
bases 980-1060 of *E. coli* 16S rRNA or the encoding DNA;  
bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;  
bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;  
bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;  
bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1440-1620 of *E. coli* 23S rRNA or the encoding DNA;  
bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; or  
bases 2190-2335 of *E. coli* 23S rRNA or the encoding DNA; and

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b) designing said oligonucleotide probe sequence so that a duplex formed between an oligonucleotide probe comprising said oligonucleotide probe sequence forms a probe:target duplex with nucleic acid from each of said two or more target species having a higher  $T_m$  than a probe:nontarget duplex formed between said oligonucleotide probe and nucleic acid from said one or more nontarget species.

421. (New) The method of claim 420, wherein said target region corresponding to either bases 65-108 of *E. coli* 5S rRNA or the encoding DNA.

422. (New) The method of claim 421, wherein said target region corresponding to bases 65-108 of *E. coli* 5S rRNA.

423. (New) The method of claim 420, wherein said target region corresponds to either bases 60-105 of *E. coli* 16S rRNA or the encoding DNA.

424. (New) The method of claim 423, wherein said target region corresponds to bases 60-105 of *E. coli* 16S rRNA.

425. (New) The method of claim 420, wherein said target region corresponds to either bases 120-150 of *E. coli* 16S rRNA or the encoding DNA.

426. (New) The method of claim 425, wherein said target region corresponds to bases 120-150 of *E. coli* 16S rRNA.

427. (New) The method of claim 420, wherein said target region corresponds to either bases 170-230 of *E. coli* 16S rRNA or the encoding DNA.

428. (New) The method of claim 427, wherein said target region corresponds to bases 170-230 of *E. coli* 16S rRNA.

429. (New) The method of claim 420, wherein said target region corresponds to either bases 405-490 of *E. coli* 16S rRNA or the encoding DNA.

430. (New) The method of claim 429, wherein said target region corresponds to bases 405-490 of *E. coli* 16S rRNA.

431. (New) The method of claim 429, wherein said first genus is *Campylobacter* and said target region corresponds to either bases 405-428 of *E. coli* 16S rRNA or the encoding DNA.

432. (New) The method of claim 431, wherein said target region corresponds to bases 405-428 of *E. coli* 16S rRNA.

433. (New) The method of claim 429, wherein said first genus is *Campylobacter* and said target region corresponds to either bases 440-470 of *E. coli* 16S rRNA or the encoding DNA.

434. (New) The method of claim 433, wherein said target region corresponds to bases 440-470 of *E. coli* 16S rRNA.

435. (New) The method of claim 420, wherein said target region corresponds to either bases 600-675 of *E. coli* 16S rRNA or the encoding DNA.

436. (New) The method of claim 435, wherein said target region corresponds to bases 600-675 of *E. coli* 16S rRNA.

437. (New) The method of claim 435, wherein said first genus is *Legionella* and said target region corresponds to either bases 630-675 of *E. coli* 16S rRNA or the encoding DNA.

438. (New) The method of claim 437, wherein said target region corresponds to bases 630-675 of *E. coli* 16S rRNA.

439. (New) The method of claim 420, wherein said target region corresponds to either bases 705-735 of *E. coli* 16S rRNA or the encoding DNA.

440. (New) The method of claim 439, wherein said target region corresponds to bases 705-735 of *E. coli* 16S rRNA.



441. (New) The method of claim 439, wherein said first genus is *Campylobacter*.

442. (New) The method of claim 440, wherein said first genus is *Campylobacter*.

443. (New) The method of claim 420, wherein said target region corresponds to either bases 820-870 of *E. coli* 16S rRNA or the encoding DNA.

444. (New) The method of claim 443, wherein said target region corresponds to bases 820-870 of *E. coli* 16S rRNA.

445. (New) The method of claim 420, wherein said target region corresponds to either bases 980-1060 of *E. coli* 16S rRNA or the encoding DNA.

446. (New) The method of claim 445, wherein said target region corresponds to bases 980-1060 of *E. coli* 16S rRNA.

447. (New) The method of claim 445, wherein said first genus is *Campylobacter* and said target region corresponds to either bases 980-1010 of *E. coli* 16S rRNA or the encoding DNA.

448. (New) The method of claim 447, wherein said target region corresponds to bases 980-1010 of *E. coli* 16S rRNA.

449. (New) The method of claim 445, wherein said first genus is *Legionella* and said target region corresponds to either bases 975-1020 of *E. coli* 16S rRNA or the encoding DNA.

450. (New) The method of claim 449, wherein said target region corresponds to bases 975-1020 of *E. coli* 16S rRNA.

451. (New) The method of claim 445, wherein said first genus is *Mycobacterium* and said target region corresponds to either bases 1025-1060 of *E. coli* 16S rRNA or the encoding DNA.

452. (New) The method of claim 451, wherein said target region corresponds to bases 1025-1060 of *E. coli* 16S rRNA.

453. (New) The method of claim 420, wherein said target region corresponds to either bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA.

454. (New) The method of claim 453, wherein said target region corresponds to bases 1125-1155 of *E. coli* 16S rRNA.

455. (New) The method of claims 453, wherein said first genus is *Salmonella*.

456. (New) The method of claims 454, wherein said first genus is *Salmonella*.

457. (New) The method of claim 420, wherein said target region corresponds to either bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA.

458. (New) The method of claim 457, wherein said target region corresponds to bases 1250-1290 of *E. coli* 16S rRNA.

459. (New) The method of claim 420, wherein said target region corresponds to either bases 270-405 of *E. coli* 23S rRNA or the encoding DNA.

460. (New) The method of claim 459, wherein said target region corresponds to bases 270-405 of *E. coli* 23S rRNA.

461. (New) The method of claim 459, wherein said first genus is *Legionella* and said target region corresponds to either bases 350-395 of *E. coli* 23S rRNA or the encoding DNA.

462. (New) The method of claim 461, wherein said target region corresponds to bases 350-395 of *E. coli* 23S rRNA.

463. (New) The method of claim 459, wherein said first genus is *Salmonella* and said target region corresponds to either bases 335-375 of *E. coli* 23S rRNA or the encoding DNA.

464. (New) The method of claim 463, wherein said target region corresponds to bases 335-375 of *E. coli* 23S rRNA.

465. (New) The method of claim 420, wherein said target region corresponds to either bases 535-575 of *E. coli* 23S rRNA or the encoding DNA.

466. (New) The method of claim 465, wherein said target region corresponds to bases 535-575 of *E. coli* 23S rRNA.

467. (New) The method of claim 420, wherein said target region corresponds to either bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA.

468. (New) The method of claim 467, wherein said target region corresponds to bases 1150-1200 of *E. coli* 23S rRNA.

469. (New) The method of claim 420, wherein said target region corresponds to either bases 1440-1620 of *E. coli* 23S rRNA or the encoding DNA.

470. (New) The method of claim 469, wherein said target region corresponds to bases 1440-1620 of *E. coli* 23S rRNA.

471. (New) The method of claim 469, wherein said first genus is *Legionella* and said target region corresponds to either bases 1585-1620 of *E. coli* 23S rRNA or the encoding DNA.

472. (New) The method of claim 471, wherein said target region corresponds to bases 1585-1620 of *E. coli* 23S rRNA.

473. (New) The method of claim 469, wherein said first genus is *Mycobacterium* and said target region corresponds to either bases 1440-1475 of *E. coli* 23S rRNA or the encoding DNA.

474. (New) The method of claim 473, wherein said target region corresponds to bases 1440-1475 of *E. coli* 23S rRNA.

475. (New) The method of claim 469, wherein said first genus is Mycobacterium and said target region corresponds to either bases 1515-1555 of *E. coli* 23S rRNA or the encoding DNA.

476. (New) The method of claim 475, wherein said target region corresponds to bases 1515-1555 of *E. coli* 23S rRNA.

477. (New) The method of claim 469, wherein said first genus is Mycobacterium and said target region corresponds to either bases 1570-1610 of *E. coli* 23S rRNA or the encoding DNA.

478. (New) The method of claim 477, wherein said target region corresponds to bases 1570-1610 of *E. coli* 23S rRNA.

479. (New) The method of claim 420, wherein said target region corresponds to either bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA.

480. (New) The method of claim 479, wherein said target region corresponds to bases 1710-1750 of *E. coli* 23S rRNA.

481. (New) The method of claim 420, wherein said target region corresponds to either bases 2190-2335 of *E. coli* 23S rRNA or the encoding DNA.

482. (New) The method of claim 481, wherein said target region corresponds to bases 2190-2335 of *E. coli* 23S rRNA.

483. (New) The method of claim 481, wherein said first genus is Legionella and said target region corresponds to either bases 2280-2330 of E. coli 23S rRNA or the encoding DNA.

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484. (New) The method of claim 483, wherein said target region corresponds to bases 2280-2330 of E. coli 23S rRNA.

485. (New) The method of any of claims 421-484, further comprising the steps of:

producing said oligonucleotide probe comprising said oligonucleotide probe sequence,

determining whether said oligonucleotide probe hybridizes to nucleic acid from each of said two or more target species under high stringency hybridization assay conditions to form a detectable probe:target duplex; and

determining whether said oligonucleotide probe hybridizes to nucleic acid from said one or more nontarget species under said conditions to form a detectable probe:nontarget duplex.